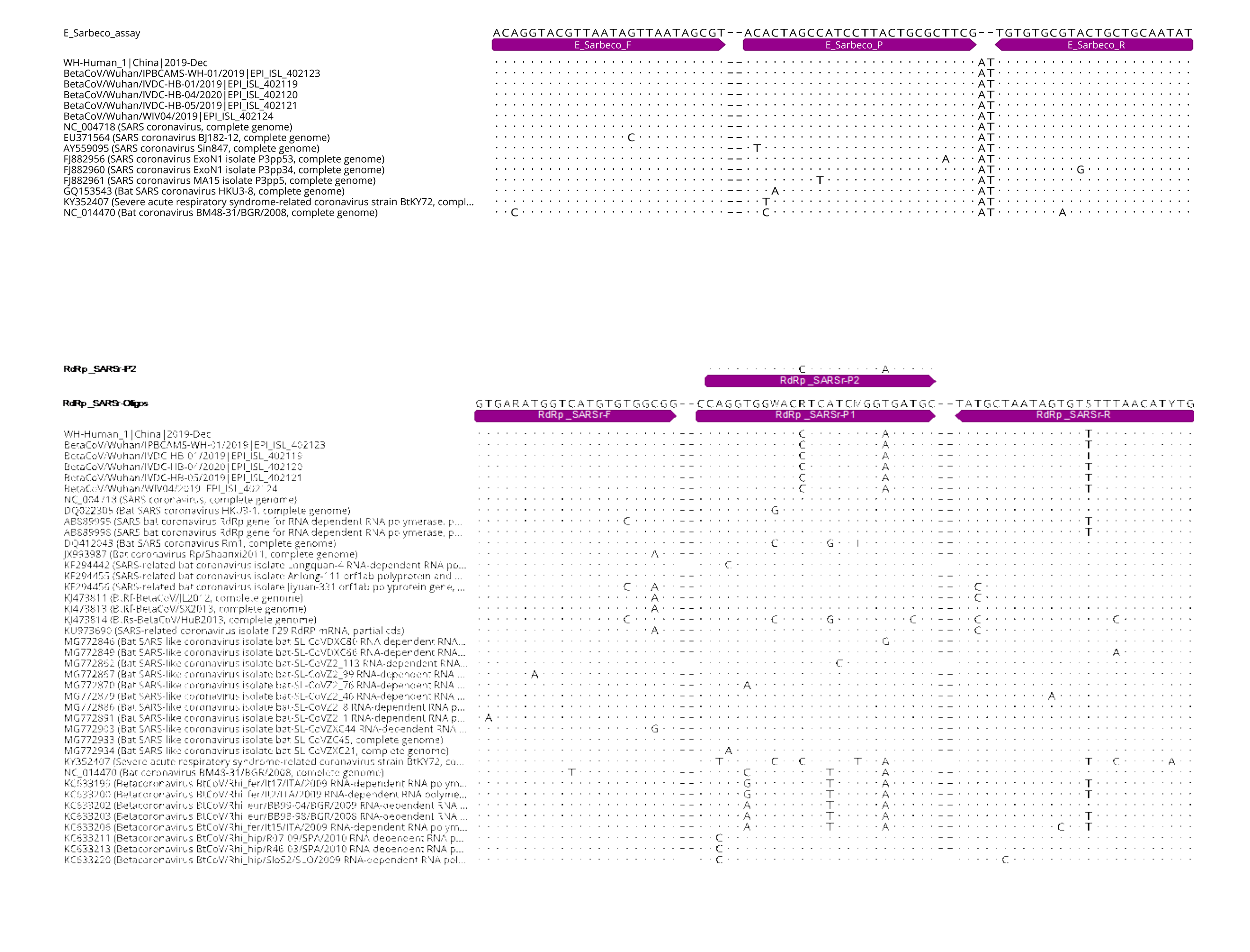
Supplementary figures, 2019 novel coronavirus RT-PCR development



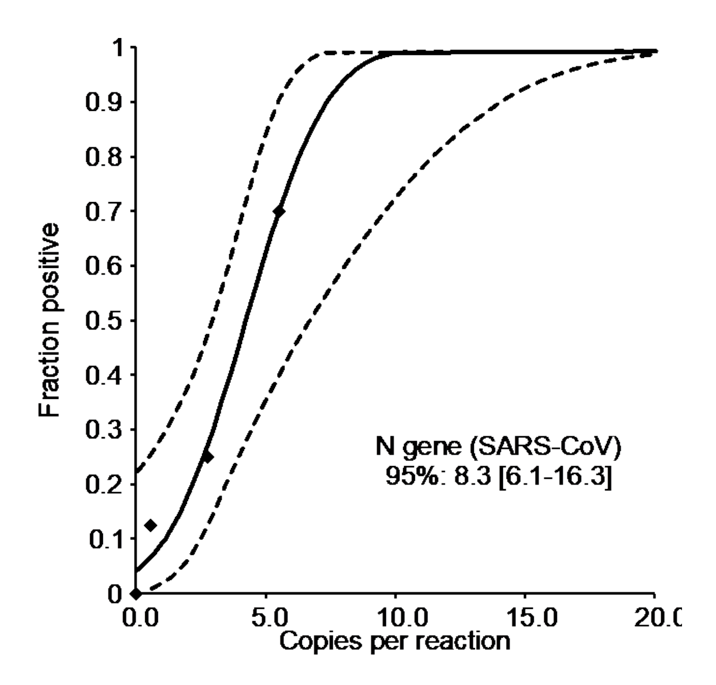
N_Sarbeco_Oligos

CACATTGGCACCCGCAATC--ACTTCCTCAAGGAACAACATTGCCA--CAAGCCTCTTCTCGTTCCTC

N_Sarbeco_F N_Sarbeco_P N_Sarbeco_R

WH-Human_1|China|2019-Dec
BetaCoV/Wuhan/IPBCAMS-WH-01/2019|EPI_ISL_402123
BetaCoV/Wuhan/IVDC-HB-01/2019|EPI_ISL_402119
BetaCoV/Wuhan/IVDC-HB-04/2020|EPI_ISL_402120
BetaCoV/Wuhan/IVDC-HB-05/2019|EPI_ISL_402121
BetaCoV/Wuhan/WIV04/2019|EPI_ISL_402124
NC_004718 (SARS coronavirus, complete genome)
DQ022305 (Bat SARS coronavirus HKU3-1, complete genome)
DQ412042 (Bat SARS coronavirus Rf1, complete genome)
EU371564 (SARS coronavirus BJ182-12, complete genome)
GQ153542 (Bat SARS coronavirus HKU3-7, complete genome)
JX162087 (SARS coronavirus ExoN1 isolate c5P10, complete genome)
JX993987 (Bat coronavirus Rp/Shaanxi2011, complete genome)
KC881005 (Bat SARS-like coronavirus RsSHC014, complete genome)
KF294457 (SARS-related bat coronavirus isolate Longquan-140 orf1ab polyprotein, s...
KJ473814 (BtRs-BetaCoV/HuB2013, complete genome)
KJ473815 (BtRs-BetaCoV/GX2013, complete genome)
KJ473816 (BtRs-BetaCoV/YN2013, complete genome)
KP886808 (Bat SARS-like coronavirus YNLF_31C, complete genome)
KY417143 (Bat SARS-like coronavirus isolate Rs4081, complete genome)
KY417144 (Bat SARS-like coronavirus isolate Rs4084, complete genome)
KY417146 (Bat SARS-like coronavirus isolate Rs4231, complete genome)
MG772933 (Bat SARS-like coronavirus isolate bat-SL-CoVZC45, complete genome)
KY352407 (Severe acute respiratory syndrome-related coronavirus strain BtKY72, co...
NC_014470 (Bat coronavirus BM48-31/BGR/2008, complete genome)

Supplementary Figure 1. Non-redundant alignments of SARS-related CoVs focused on oligonucleotide binding sites of all assays (top to bottom: RdRp, E, N). Viruses not present in these alignments have been removed because their binding sites are 100% identical to one of the members of the alignment. ("--") means sequence gaps not covered by oligonucleotides.



Supplementary Figure 2: Additional confirmatory assay: N gene. Limit of detection study for N gene assay. Technical LOD = 8.3 RNA copies/reaction, at 95% hit rate; 95% CI: 6.1-16.3 RNA copies/reaction. Y-axis shows positive results in all parallel reactions performed, squares are experimental data points resulting from replicate testing of given concentrations (x-axis) in parallels assays (8 replicate reactions per datum point). The inner line is a probit curve (dose-response rule). The outer dotted lines are 95% confidence intervals.